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FIG. 1A

5'	11			20			29			38			47			56		
	GAG	ACT	CAC	GGT	CAA	GCT	AAG	GCG	AAG	AGT	GGG	TGG	CTG	AAG	CCA	TAC	TAT	TTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	65			74			83			92			101			110		
	ATA	GAA	TTA	ATG	GAA	AGC	AGA	AAA	GAC	ATC	ACA	AAC	CAA	GAA	GAA	CTT	TGG	AAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
				M	E	S	R	K	D	I	T	N	Q	E	E	L	W	K
	119			128			137			146			155			164		
	ATG	AAG	CCT	AGG	AGA	AAT	TTA	GAA	GAA	GAC	GAT	TAT	TTG	CAT	AAG	GAC	ACG	GGA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	M	K	P	R	R	N	L	E	E	D	D	Y	L	H	K	D	T	G
	173			182			191			200			209			218		
	GAG	ACC	AGC	ATG	CTA	AAA	AGA	CCT	GTG	CTT	TTG	CAT	TTG	CAC	CAA	ACA	GCC	CAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	E	T	S	M	L	K	R	P	V	L	L	H	L	H	Q	T	A	H
	227			236			245			254			263			272		
	GCT	GAT	GAA	TTT	GAC	TGC	CCT	TCA	GAA	CTT	CAG	CAC	ACA	CAG	GAA	CTC	TTT	CCA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	A	D	E	F	D	C	P	S	E	L	Q	H	T	Q	E	L	F	P
	281			290			299			308			317			326		
	CAG	TGG	CAC	TTG	CCA	ATT	AAA	ATA	GCT	GCT	ATT	ATA	GCA	TCT	CTG	ACT	TTT	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Q	W	H	L	P	I	K	I	A	A	I	I	A	S	L	T	F	L
	335			344			353			362			371			380		
	TAC	ACT	CTT	CTG	AGG	GAA	GTA	ATT	CAC	CCT	TTA	GCA	ACT	TCC	CAT	CAA	CAA	TAT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Y	T	L	L	R	E	V	I	H	P	L	A	T	S	H	Q	Q	Y
	389			398			407			416			425			434		
	TTT	TAT	AAA	ATT	CCA	ATC	CTG	GTC	ATC	AAC	AAA	GTC	TTG	CCA	ATG	GTT	TCC	ATC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	F	Y	K	I	P	I	L	V	I	N	K	V	L	P	M	V	S	I
	443			452			461			470			479			488		
	ACT	CTC	TTG	GCA	TTG	GTT	TAC	CTG	CCA	GGT	GTG	ATA	GCA	GCA	ATT	GTC	CAA	CTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	T	L	L	A	L	V	Y	L	P	G	V	I	A	A	I	V	Q	L
	497			506			515			524			533			542		
	CAT	AAT	GGA	ACC	AAG	TAT	AAG	AAG	TTT	CCA	CAT	TGG	TTG	GAT	AAG	TGG	ATG	TTA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	H	N	G	T	K	Y	K	K	F	P	H	W	L	D	K	W	M	L
	551			560			569			578			587			596		
	ACA	AGA	AAG	CAG	TTT	GGG	CTT	CTC	AGT	TTC	TTT	TTT	GCT	GTA	CTG	CAT	GCA	ATT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	T	R	K	Q	F	G	L	L	S	F	F	F	A	V	L	H	A	I
	605			614			623			632			641			650		
	TAT	AGT	CTG	TCT	TAC	CCA	ATG	AGG	CGA	TCC	TAC	AGA	TAC	AAG	TTG	CTA	AAC	TGG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Y	S	L	S	Y	P	M	R	R	S	Y	R	Y	K	L	L	N	W

659	668	677	686	695	704
GCA TAT CAA CAG GTC	CAA CAA AAT	AAA GAA GAT	GCC TGG ATT	GAG CAT GAT	GTT
A Y Q Q V	Q Q N	K E D	A W I	E H D	V
713	722	731	740	749	758
TGG AGA ATG GAG ATT	TAT GTG TCT	CTG GGA ATT	GTG GGA TTG	GCA ATA CTG	GCT
W R M E I	Y V S	L G I	V G L	A I L	A
767	776	785	794	803	812
CTG TTG GCT GTG ACA TCT	ATT CCA TCT	GTG AGT GAC	TCT TTG ACA	TGG AGA GAA	
L L A V T	S I P	S V S	D S L	T W R	E
821	830	839	848	857	866
TTT CAC TAT ATT CAG	AGC AAG CTA	GGA ATT GTT	TCC CTT CTA	CTG GGC ACA	ATA
F H Y I Q	S K L	G I V	S L L	L G T	I
875	884	893	902	911	920
CAC GCA TTG ATT TTT	GCC TGG AAT	AAG TGG ATA	GAT ATA AAA	CAA TTT GTA	TGG
H A L I F	A W N	K W I	D I K	Q F V	W
929	938	947	956	965	974
TAT ACA CCT CCA ACT	TTT ATG ATA	GCT GTT TTC	CTT CCA ATT	GTT GTC CTG	ATA
Y T P P T	F M I	A V F	L P I	V V L	I
983	992	1001	1010	1019	1028
TTT AAA AGC ATA CTA	TTC CTG CCA	TGC TTG AGG	AAG AAG ATA	CTG AAG ATT	AGA
F K S I L	F L P	C L R	K K I	L K I	R
1037	1046	1055	1064	1073	1082
CAT GGT TGG GAA GAC	GTC ACC AAA	ATT AAC AAA	ACT GAG ATA	TGT TCC CAG	TTG
H G W E D	V T K	I N K	T E I	C S Q	L
1091	1100	1109	1118	1127	1136
TAG AAT TAC TGT TTA	CAC ACA TTT	TTG TTC AAT	ATT GAT ATA	TTT TAT CAC	CAA
* N Y C L H	T F L	F N I	D I F	Y H Q	
1145	1154	1163	1172	1181	1190
CAT TTC AAG TTT GTA	TTT GTT AAT	AAA ATG ATT	ATT CAA GGA	AAA AAA AAA	AAA
H F K F V	F V N	K M I	I Q G	K K K	K

AAA AA 3'

K

FIG. 1B

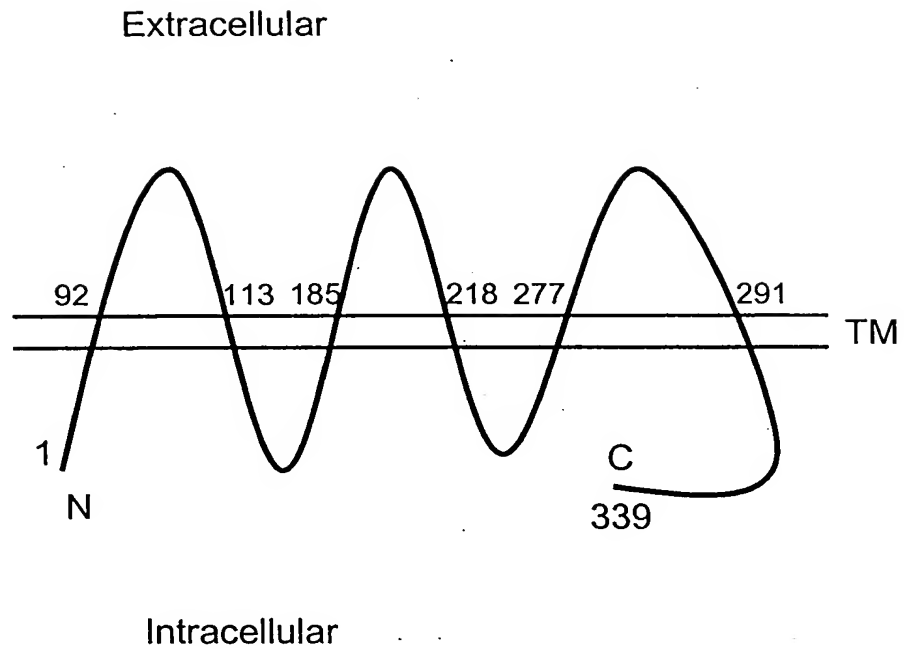
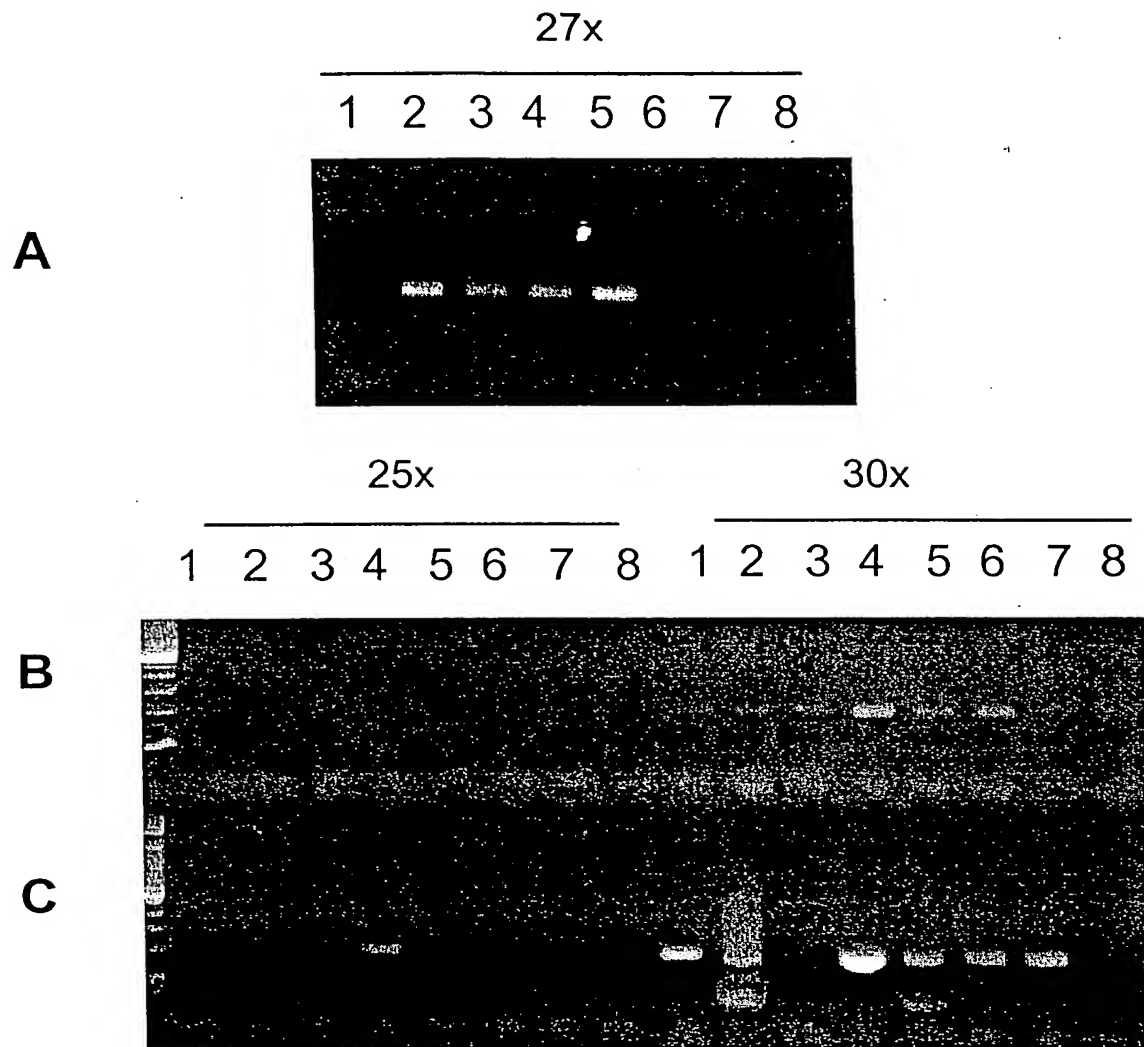


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3'

FIG. 2



Panels:

A

1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

B

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

C

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 3A

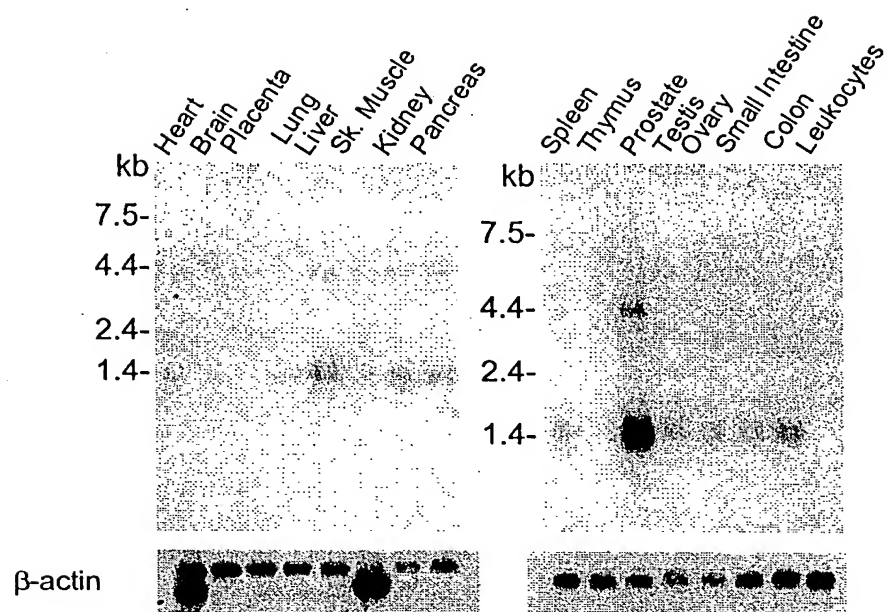


FIG. 3B

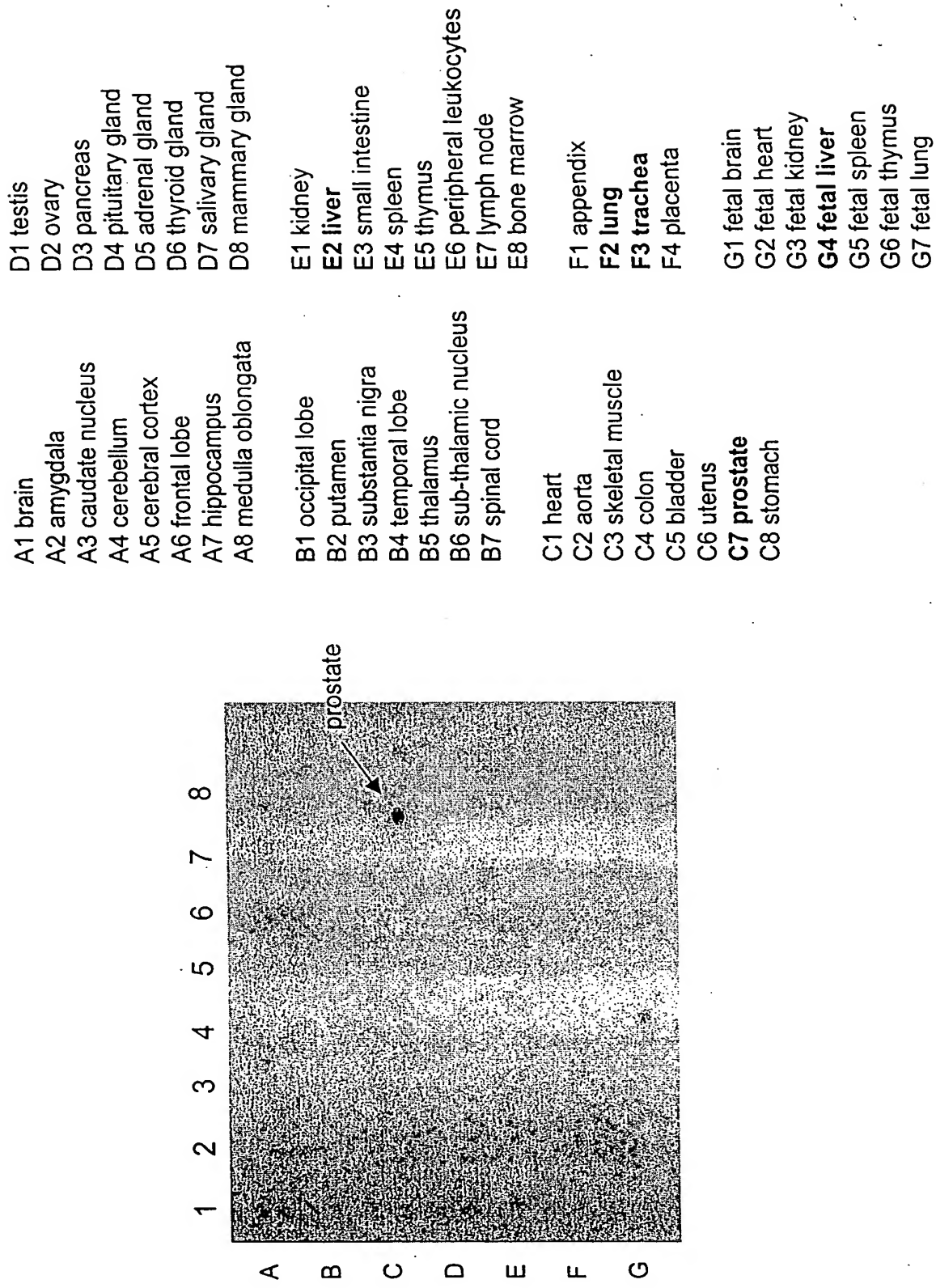


FIG. 4

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACCTTTCCACA
GTGGCACTTGCCAATTAATAAGCTGCTATTATAGCATCTCTGACTTTTCTTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGCCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAATTTCACTATATTCAAGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCTTAGACATAAAATAAAGGCAT
TAAAAATATCTTTGTTTTTTTTTTTTTGTGTTGTTGTTTTTGTGTTGTTGTTGTTTTTGTGAGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTTCAGGCGATTCT
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTGTATTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTAGGAATCCAATATGCATGGTTTATTATTCTTAAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCCAGAAACAAAACTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTCCAGCTTACATTTTATAT
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCTAATTTGTAGGTTTCAG
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTACACATATGA
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACCTGAGCCTATTCTACTATATGTACA

ATACCTAGCCCATAAATAGGTATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA
ACGCAAACTTAGCTATTTGATTGTATTCCTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTGAGAACACCGT
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACCTGATAAAGATCACTGAAGTCAAATGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAATGTACAAATCATTGTGTTGATTCTGCAGTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTTTTCTTTTGAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG
ATATGTTCCAGTTGAGAAATTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCA
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA

FIG. 5

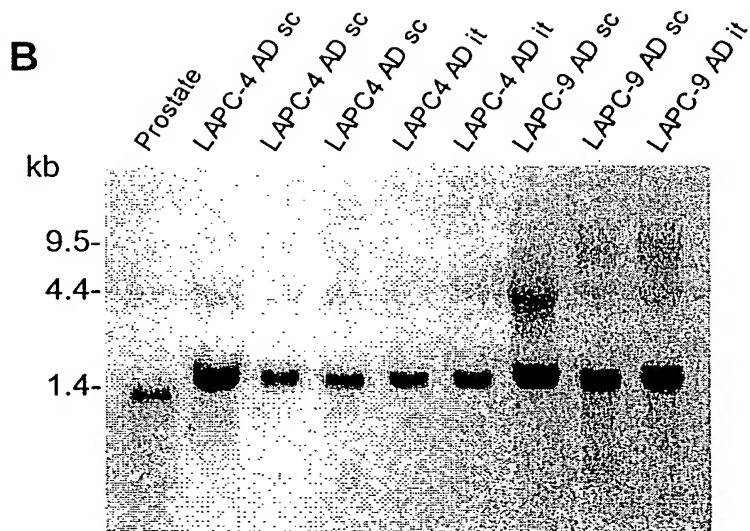
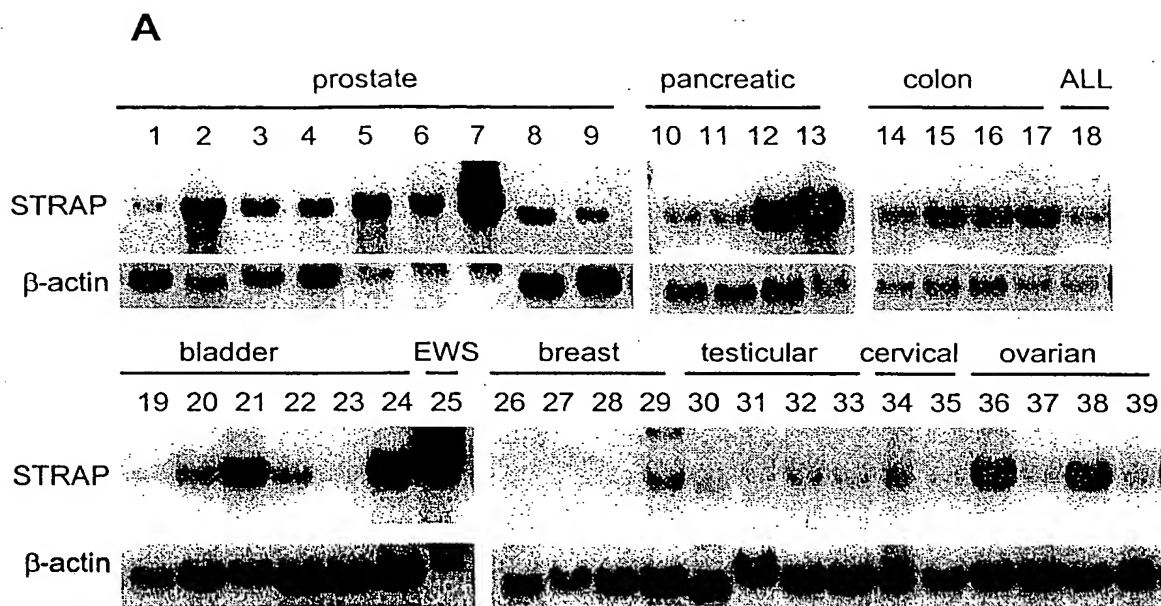


FIG. 6

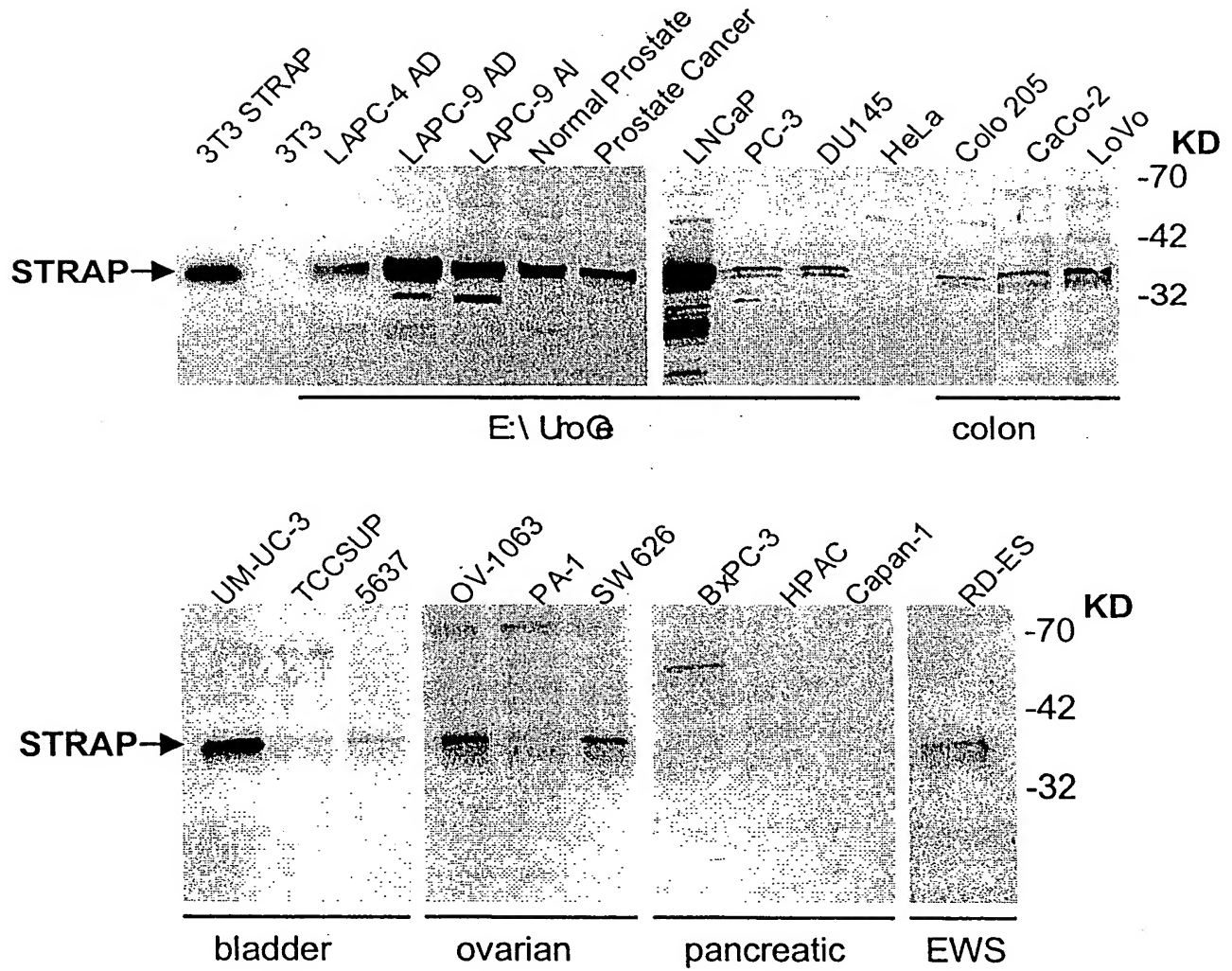
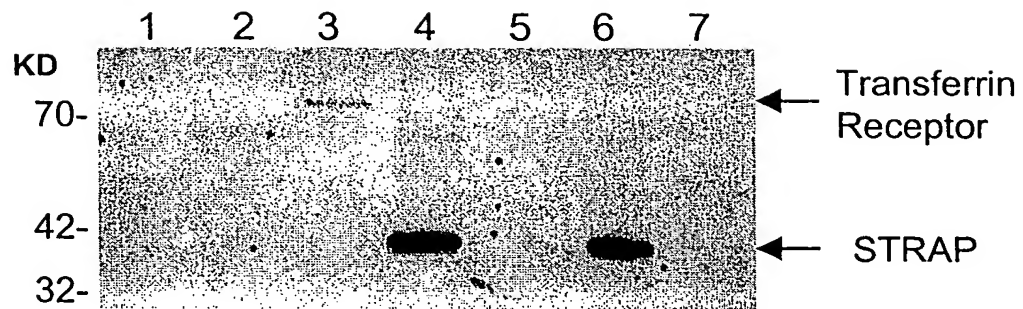


FIG. 7

A



B

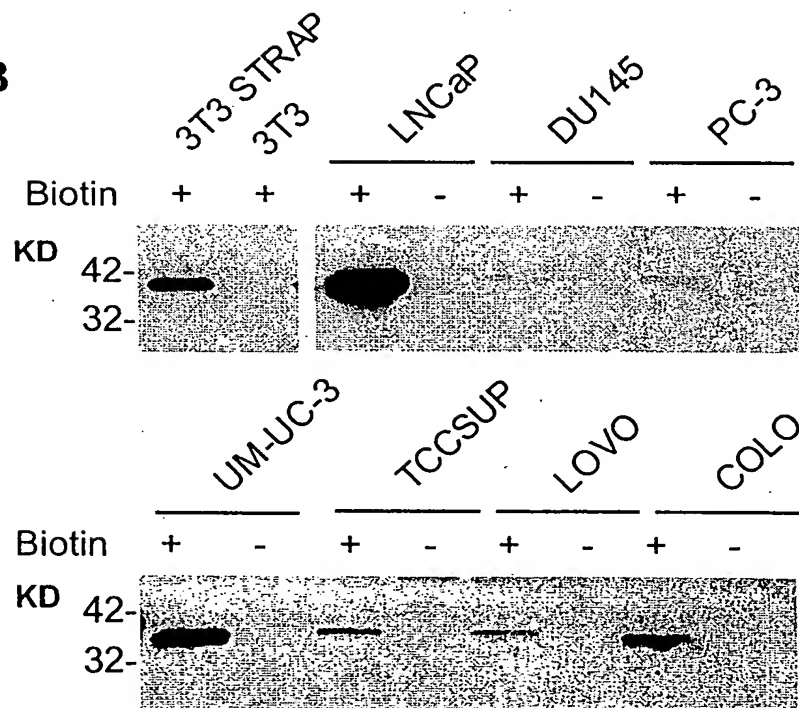


FIG. 8

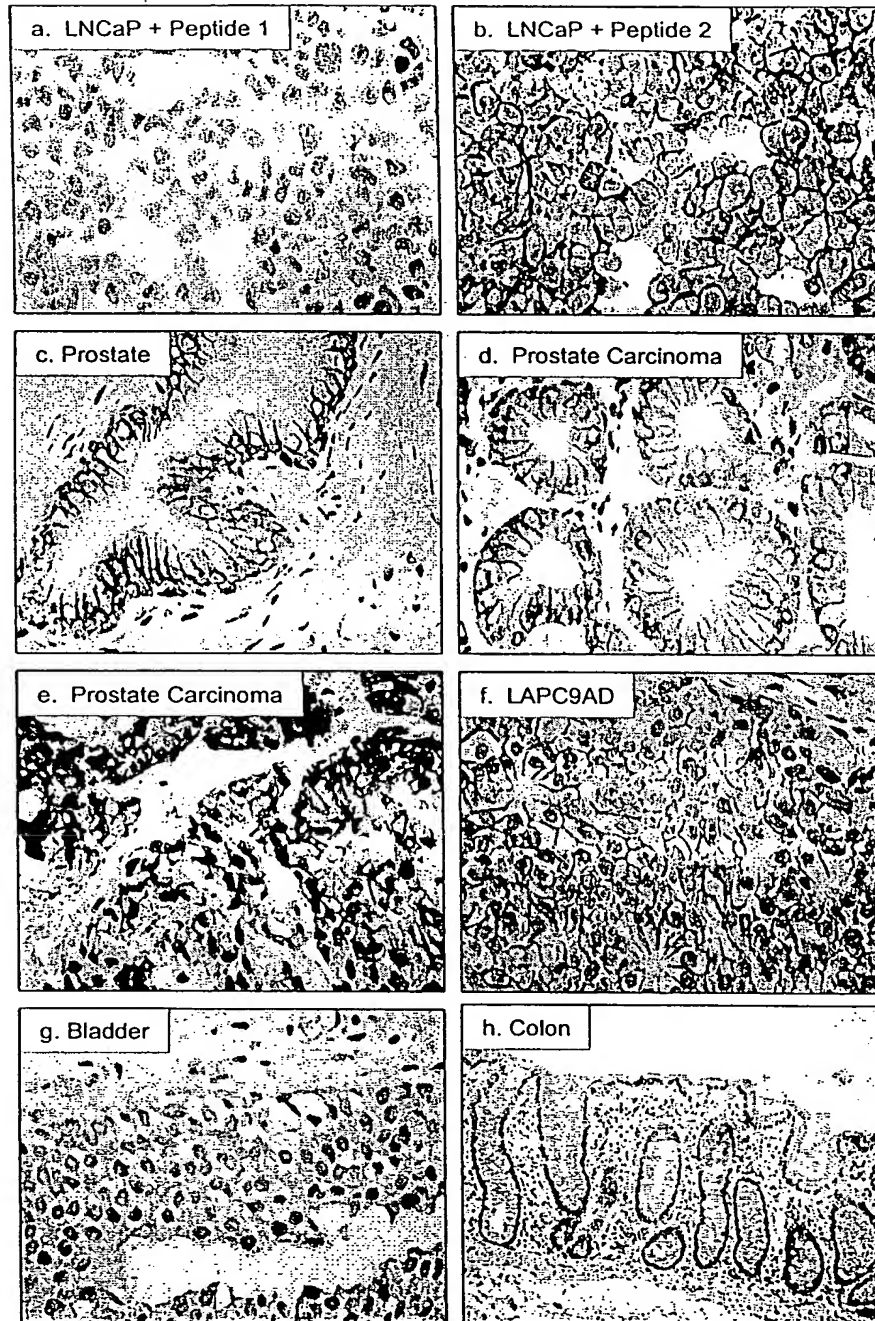


FIG. 9

```

      10      19      28      37      46      55
5'  GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    ---
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

      64      73      82      91      100      109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118      127      136      145      154      163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172      181      190      199      208      217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226      235      244      253      262      271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280      289      298      307      316      325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334      343      352      361      370      379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388      397      406      415      424      433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442      451      460      469      478      487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496      505      514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3'
    ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala

```

FIG. 10

STRAP-2, AA508880 (NCI_CGAP Pr6)

ggtcgacttttccctttattcctttgtcagagatctgattcatccatattgctagaaaccaacagagtgactttttaca
aaattccctatagagattgtgaataaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttggttggaacctgggta
cagtgtagaaaacagcttggattactaagtgtgttcttcgctatgggtccatgttgcctacagcctctgcttaccga
tgagaaggtcagagagat

STRAP-2, 98P4B6 SSH fragment

TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCTATTGACTCTACTTCTTTAAAGCG
GCTGCCCATTACATTCTCAGCTGTCTTGAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
TCCTCAAAGGAAGGCAGCATGTGTCCTTTTT

AI139607 (testis EST)

aagaaggagaatccatttagcacctcctcagcctggctcagtgattcatatgtggctttgggaataacttgggtttt
ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcaactggagagagttccgatttgt
ccagtcctaaactgggttatttgacctgatcttgtgtacagccacacccctgggtgtacggtgggaagagattcctc
agcccttcaaatctcagatgggtatcttctgcagcctacgtgttagggcttatcattccttgcactgtgctgggtga
tcaagtttgtcctaatacatgccatgtgtagacaacacccttacaaggatccgccagggtgggaaaggaactcaaa
acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaaa

R80991 (placental EST)

ggccgcggcancgcgtacgacctgggtcaacctggcagtcgaagcaggtcttggccanacaagagccacctctgggtg
aaggaggaggtctggcggttgagatctacctctccctgggagtgctggccctcggcacgttgtccctgctggcg
tgacctcactgccgtccattgcaaaactcgtcaactggagggagttcagcttcgttcagtcctcactgggctttgt
ggccttcgtgctgagcacactncacacgctcacctacggctggacccgcgccttcgaggagagccgctacaagttc
tacctncctcccaccttcacgntcacgctgctggtgccttgcttcgttcacctcctgggcaaaagccctgtttntac
tgcccttgcatcagccgnaga

FIG. 11A

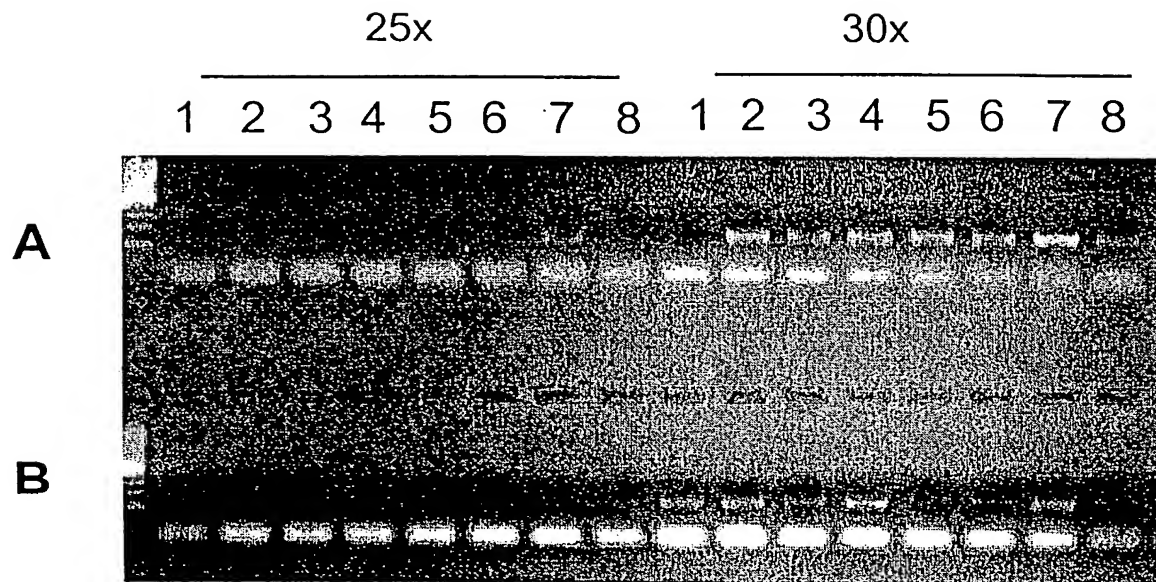
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STRAP-1 106 FYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STRAP-2 2 FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPWPWLETWLQCRKQLG
          ***** ** ** * ***** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** ** **
          ***** ** ** * ***** ** ** ** ** ** ** ** ** ** ** ** ** **

STRAP-1 166 LLSFFFAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
STRAP-2 62 LLSFFFAMVHVAYSLCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIM
          ***** * *** ***** ** ** ***** ** ** * * ** * * * * *

STRAP-1 226 GLAILALLAVTSIPSVDSL TWREFHYIQSKLGIVSLLGTIHALIFAWNK
STRAP-2 122 SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
          * * ***** * ***** ** ** * * * * * * * *
```

1	15 16	30 31	45 46	60 61	75 76	90
STRAP-1	MESKXDIITNOBELWK	MKPRRNLEEDDYLHK	DTGETSMLKRPVLLH	LHOTAHADEFDPCSE	LQHTQELFPQWHLPI	KIAAIIASLFLYTL
STRAP-2	-----	-----	-----	-----	-----	-----
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
91	105 106	120 121	135 136	150 151	165 166	180
STRAP-1	LREVIHPLATSHQQY	FYKIPITLVNKVLEPM	VSITLGLAVYIPGVIT	AAIVOLHNVTIKYKKF	PHWLDKMWLTKRQFG	DLSEFFFAVLHAIYSZ
STRAP-2	-----D	FYKIPITLVNKVLEPI	VAITLUSLVYDAAGL	AAAYOLYYTUKYRRF	EPWDEITWLOCRKQIG	DLSEFFFAVHVAYSZ
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
181	195 196	210 211	225 226	240 241	255 256	270
STRAP-1	SYPMKRSRYKULDNW	AYOOVQONKEDAWIE	HDVWRMEIYVSGLIV	GLAIIALLAVTSPIS	VSDSLTWREHFHYIQS	KUGIVSDDLGTHIAL
STRAP-2	CIPMKRSERYLFLNW	AYOOVHANIENTSWNE	EEVWRLEMTISFGIM	SLGLSLGLAVTSPIS	VSNALNWRREFSEFIQS	TUGYVALLGISTFAVL
STRAP-3	-----	-----KKNPFST	SSAWLSDSYVALGIL	GFPLFVLDGITSDFS	VSNVAVNWRREFSEFVQS	KUGYLTLLIQTAAHVL
STRAP-4	-----ATTWSIW	QSSRSWPXXKSHLWK	EEVWRMEIYLSLGLIV	ALGTLSDGLAVTSPIS	IANSIINWRREFSEFVQS	SLGFWAVVLSLTHLVL
271	285 286	300 301	315 316	330 331	345 346	360
STRAP-1	IFAWNKWIDIKQFVW	YTPPTFMIAVFLPIV	VLLTFKSILFIPCTIRK	KILIRHGWEDVTKI	NKTEICSQL	339
STRAP-2	IYGNKRA	-----	-----	-----	-----	173
STRAP-3	YVGGKRFLLSPSNLRW	YLPAAVVLGLIIPCT	VZVIKFLVLIIMPVDPN	TLIRIQOGWERNSKH	-----	128
STRAP-4	TYGWTRAFEEESRYKF	YLPFTTITXTLLVPV	RSSWAKALEXLPICQ	P-----	-----	128

FIG. 12



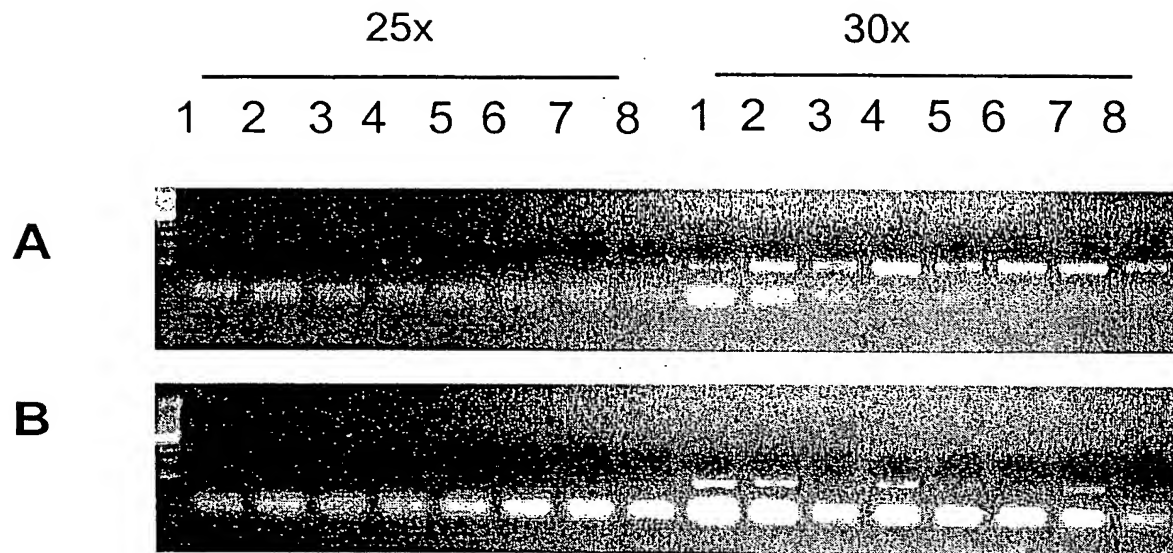
A

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 13



A

1. Brain
2. Heart
3. Kidney
4. Liver
5. Lung
6. Pancreas
7. Placenta
8. Skeletal Muscle

B

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG.14

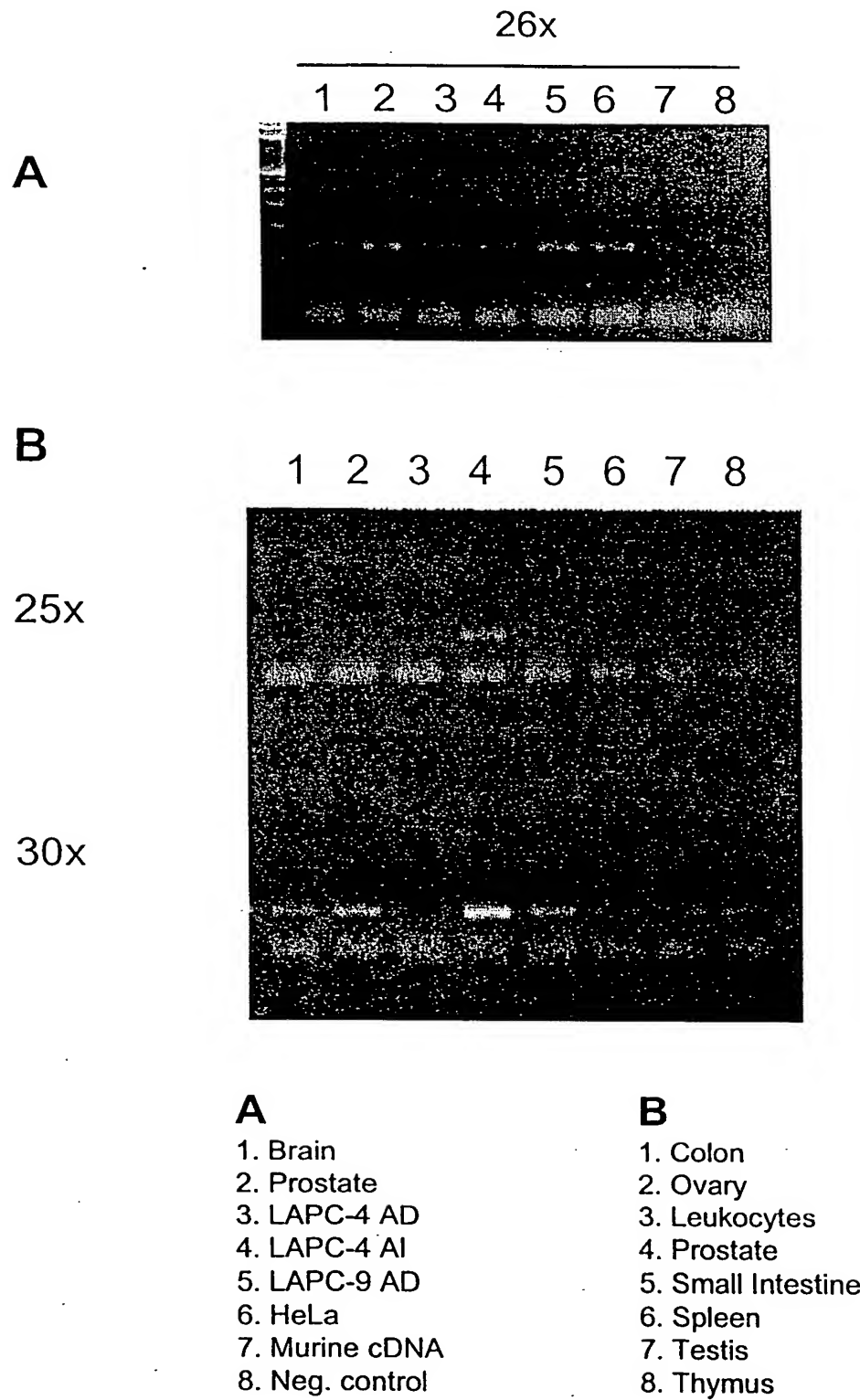


FIG. 15

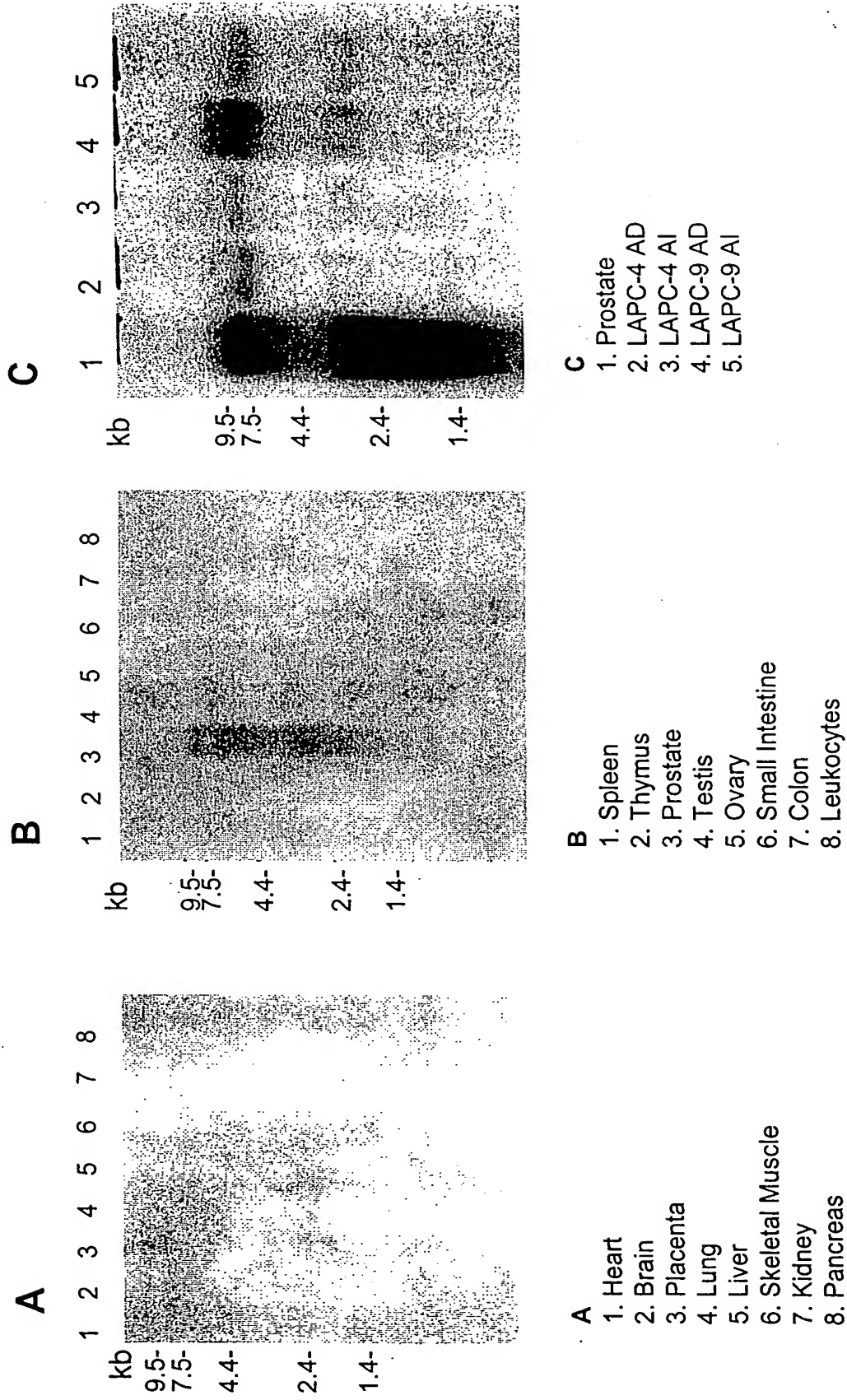


FIG. 16

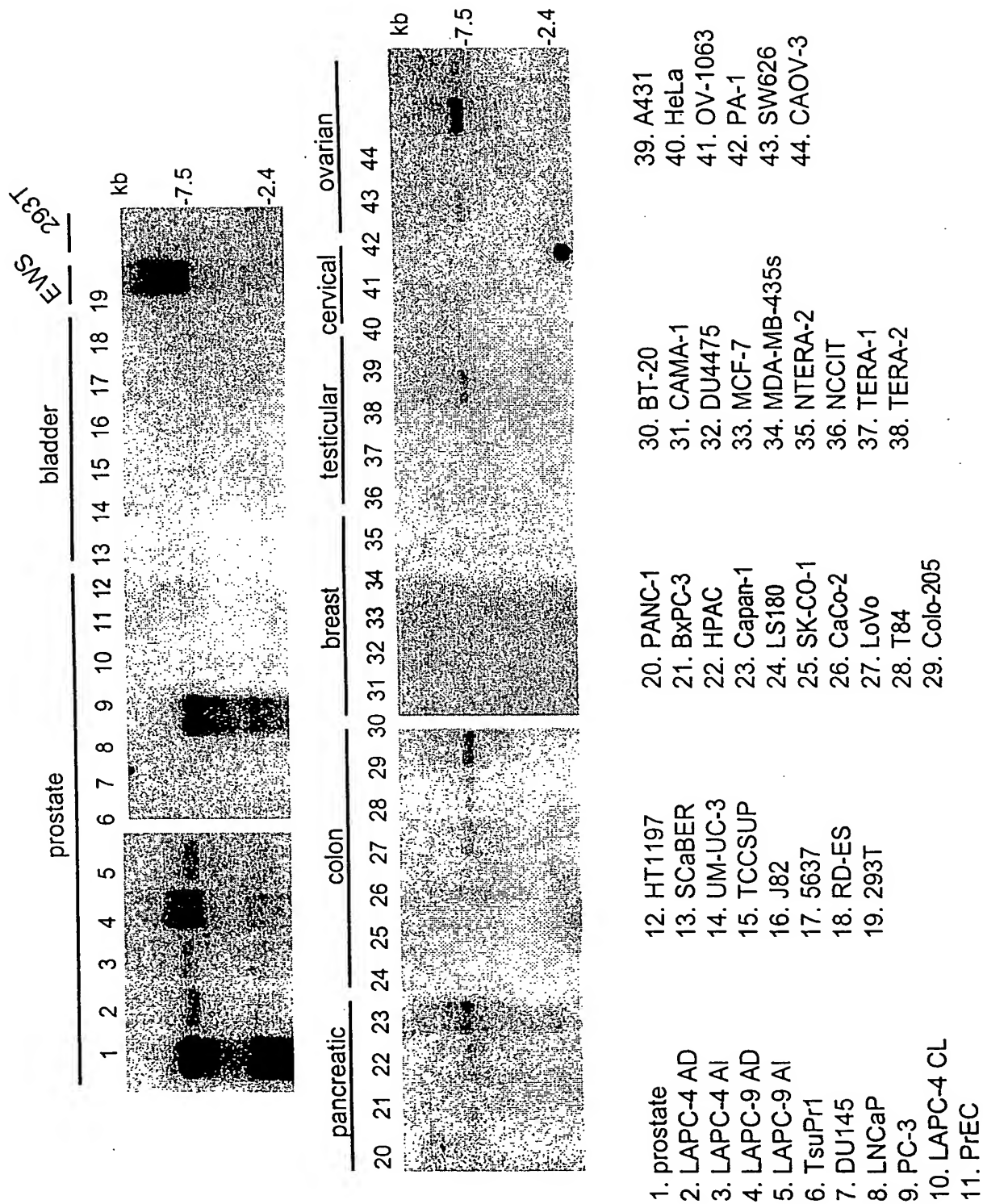


FIG. 17

GDB Compreher

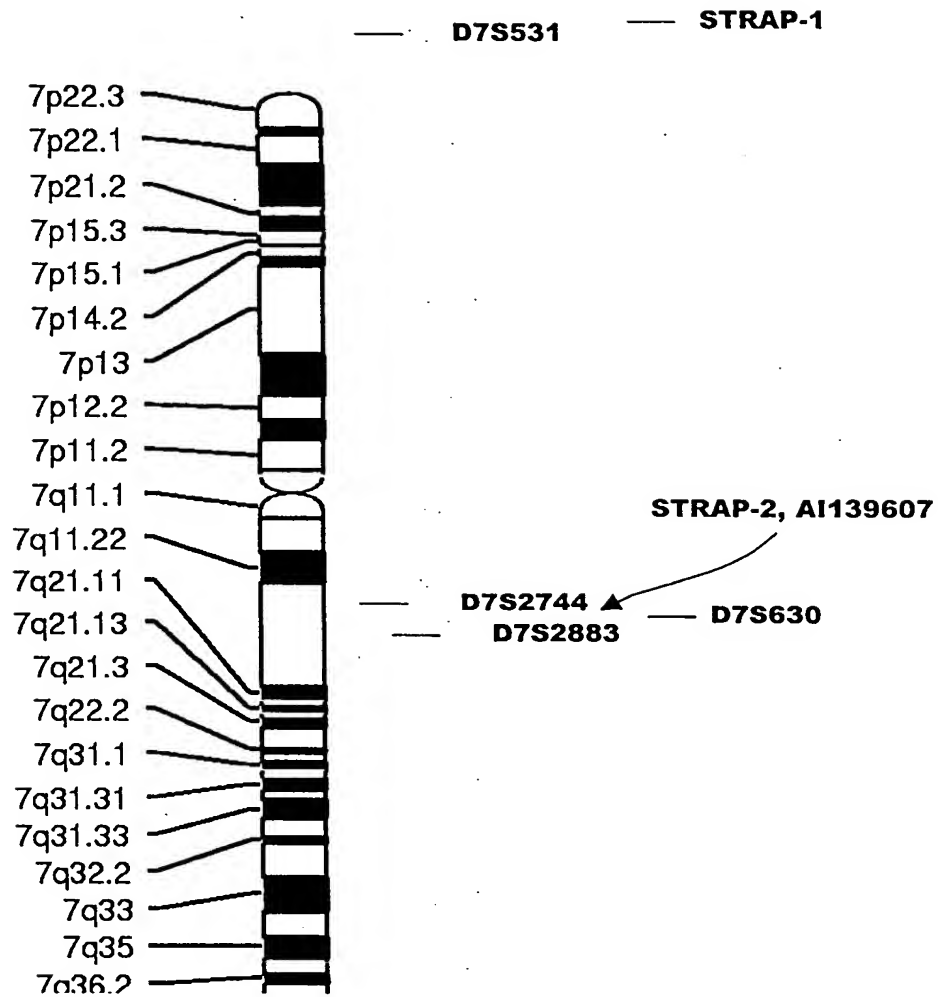


FIG. 18

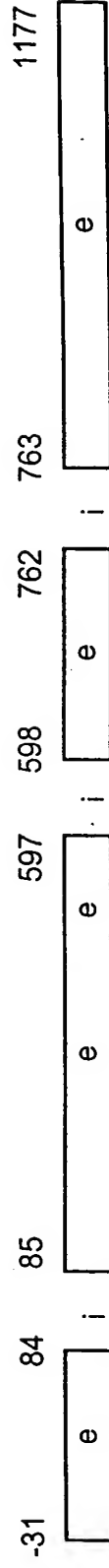


FIG. 19

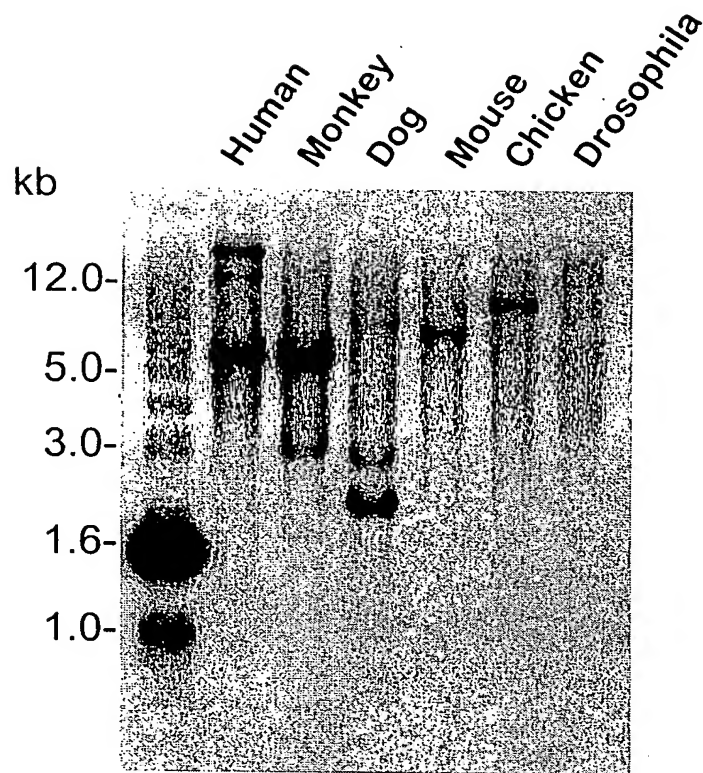
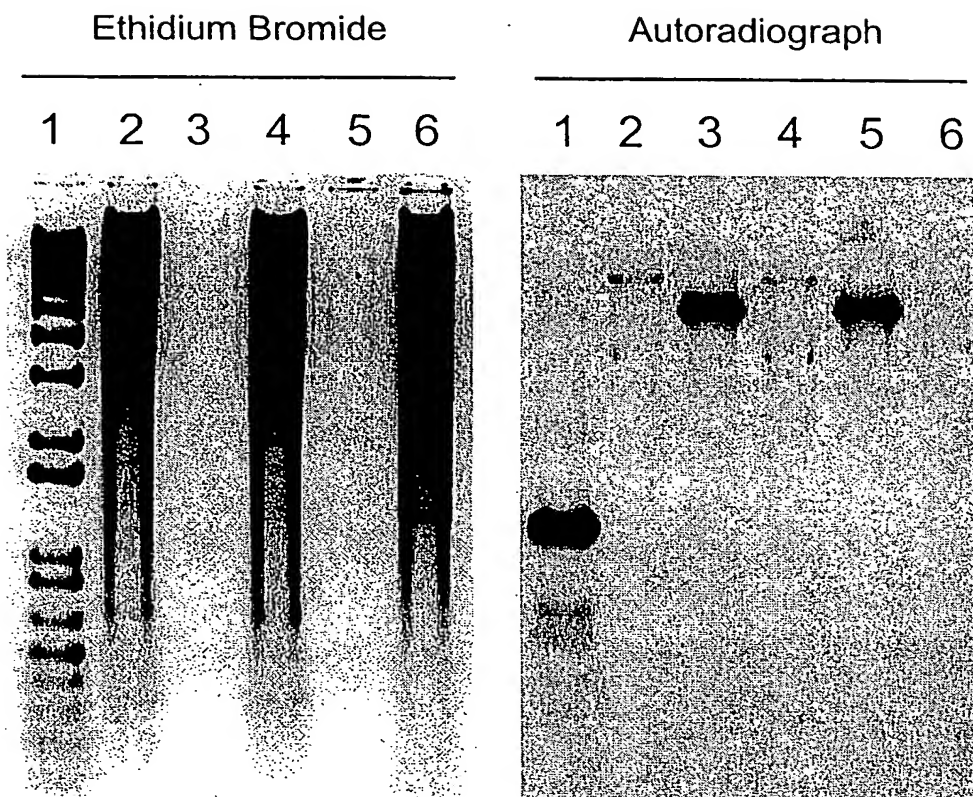


FIG. 20



Lanes

- 1) 1kb ladder
- 2) human female genomic
- 3) 12P11 BAC mus
- 4) human female genomic
- 5) 12P11 BAC mus
- 6) 3T3